Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-19 (cancelled)

20. (New) A method of screening for altered immunogenicity of a target protein comprising an immunogenic sequence selected from the group consisting of sequences that bind to MHC class I molecules, MHC class II molecules, T cell epitopes or B cell epitopes; said method comprising:

a) inputting the coordinates of said target protein into a computer;

b) computationally generating a set of primary variant amino acid sequences using at least two scoring functions;

c) applying a computational immunogenicity filter against said set to identify members of said set that have at least one variant immunogenic sequence;

d) synthesizing a plurality of variant proteins each comprising at least one of said variant immunogenic sequences; and,

e) selecting a variant protein with altered immunogenicity.

21. (New) A method according to Claim 20, further comprising classifying each variable residue position as either a core, surface or boundary residue.

22. (New) A method according to Claim 20, wherein said computationally generating step comprises a DEE computation.

23. (New) A method according to Claim 22, wherein said DEE computation is selected from the group consisting of original DEE and Goldstein DEE.

24. (New) A method according to Claim 20, wherein said set of primary variant amino sequences optimized for at least one scoring function comprises the globally optimal protein sequence.

25. (New) A method according to Claim 20, wherein one of said scoring functions is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic salvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

26. (New) A method according to Claim 20, wherein said computationally generating step includes the use of a Monte Carlo search.

27. (New) A method according to Claim 20, wherein said target protein is from a non human species and said candidate variant protein exhibits reduced immunogenicity in humans.

28. (New) A method according to Claim 20, wherein the immunogenicity of said candidate variant protein is reduced relative to said target protein.

29. (New) A method according to Claim 20, wherein said candidate variant protein is substantially non-immunogenic.

30. (New) A method according to Claim 1, wherein at least one of said variant immunogenic sequences is a sequence that binds to MHC class I molecules.

31. (New) A method according to Claim 1, wherein at least one of said variant immunogenic sequences is a sequence that binds to MHC class II molecules.

32. (New) A method according to Claim 1, wherein at least one of said variant immunogenic sequences is a sequence that binds to T cell epitopes.

33. (New) A method according to Claim 1, wherein at least one of said variant immunogenic sequences is a sequence that binds to B cell epitopes.